CLAIMS

What is claimed is:

1. A method of transcriptional profiling comprising:

subjecting a biological sample to an exogenous stimulation;

measuring transcriptional activity of the biological sample at a first differentiation stage;

measuring transcriptional activity of the biological sample at a second differentiation stage; and

comparing the transcriptional activities from the first and second differentiated stages in at least 5 Mbases, 50 Mbases or 100 Mbases of the genome to obtain a transcription profile.

2. The method of claim 1 wherein the measuring comprises obtaining polyA+ enriched cytosolic RNA and hybridizing the RNA to high density oligonucleotide probe arrays.

3. The method of Claim 2 wherein the oligonucleotide probe array contains at least 100,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

4. The method of Claim 3 wherein the oligonucleotide probe array contains at least 500,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

5. The method of Claim 4 wherein the oligonucleotide probe array contains at least 800,000 oligonucleotide probes, each targeting a transcript sequence from a different region of a genome.

6. The method of Claim 5 wherein oligonucleotide array further comprises mismatch (MM) probes, wherein each of the mismatch probes is different from a perfect match (PM) probe in one base.

7. The method of Claim 6 wherein the mismatch probe is different from the perfect match probe in a middle position.

8. The method of claim 7 wherein the biological sample is responsive to an exogenous stimulation.

9. The method of claim 8 wherein the biological sample is a developmentally pluripotent human germ cell tumor-derived cell line.